

## SEQUENCE LISTING

<110> Sprecher, Cindy A.  
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 <151> 2000-06-26

<150> US 60/214,955  
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 <151> 2001-08-02

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Trp Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu	
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Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr	
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agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc agt tat	320
Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr	
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Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp	
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Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser	
70 75 80	

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Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu			
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tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc cag caa gat			1328
Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp			
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Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu			
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cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa			1424
His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu			
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ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg			1472
Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val			
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Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys			
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ccc ttc agg cct gat tgt ccc ctg ggg aaa agt ttt gag gag ctc cca Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu Leu Pro 645 650 655	2144
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Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys 50 55 60	
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser 65 70 75 80	
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile 85 90 95	

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr  
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 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe  
 115 120 125  
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp  
 130 135 140  
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu  
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 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala  
 165 170 175  
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln  
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 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser  
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 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu  
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 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln  
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 Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val  
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 355 360 365  
 Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln  
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 385 390 395 400  
 Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala  
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 Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly  
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 Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly  
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 Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys  
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 625 630 635 640  
 Thr Cys Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu  
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 Leu Pro Val Ser Pro Glu Ile Pro Pro Arg Lys Ser Gln Tyr Leu Arg  
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 Ser Arg Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu  
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 Phe Ser Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala  
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ttyggngara	arcaygayaa	ytgyacnacn	aaywsnwsna	cnwsngaraa	ymgngcnwsn	240
tgywsnttyt	tyytnccnmg	nathacnath	ccngayaayt	ayacnathga	rftngargcn	300
garaayggng	ayggngtnat	haarwsncay	atgacntayt	ggmgnytnga	raayathgcn	360
aaracngarc	cnccnaarat	httymgngt	aarcngtny	tnggnathaa	rmgnatgath	420
carathgart	ggathaarc	ngarytngcn	ccngtnwsnw	sngaytnaa	rtayacnytn	480
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gayaaraayc	aracntayaa	yytnacnggn	ytnccrcnt	tyacngarta	ygttnathgcn	600
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gtgttggccc accgttccca accctgtgtc gaggatata gcccacacggc atggagatga	1200
tttcaaggat aagctaaacc tgaaggatgc tggatgtct gtgaacacag aagacaggat	1260
cttaaaaacca tggccatccc ccagtgcacaa gttgggtgatt gacaagttgg tggtaactt	1320
tgggaatgtt ctgcaagaaa tttcacaga tgaaggccaga acgggtcagg aaaacaattt	1380
aggagggaa aagaatgggaa ctagaattct gtcttcctgc ccaacttcaa tataagtgtg	1440
gactaaaatg cgagaaaggt gtcctgtggt ctatgcaaat tagaaaggac atgcagagtt	1500
ttccaacttag gaagactgaa tctgtggccc caagagaacc atctctgaag actgggtatg	1560

tggcttttc cacacatgga ccacccatcg atgtaatctg taatgcgtgt gcatgagaag 1620  
 tctgttatta agtagaggtgt gaaaacatgg ttatggtaat aggaacagct tttaaaatgc 1680  
 tttgcattt gggccttca tacaaaaaaag ccataatacc atttcgtgt aatgctatac 1740  
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 aaaacattct ctctccccag ctttcgtgt ttaacctggg g atg atg tgg acc tgg 176  
 Met Met Trp Thr Trp  
 1 5  
  
 gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224  
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu  
 10 15 20  
  
 cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272  
 Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn  
 25 30 35  
  
 tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320  
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr  
 40 45 50  
  
 aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368  
 Thr Val Lys Arg Thr Ala Phe Gly Glu Lys His Asp Asn Cys Thr  
 55 60 65  
  
 acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt 416  
 Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu  
 70 75 80 85  
  
 cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa 464  
 Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu  
 90 95 100  
  
 aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag 512  
 Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu  
 105 110 115  
  
 aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt 560  
 Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val  
 120 125 130  
  
 ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg 608  
 Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu  
 135 140 145  
  
 gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc 656  
 Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val  
 150 155 160 165

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Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp			
170	175	180	
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat	752		
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr			
185	190	195	
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac	800		
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp			
200	205	210	
tgg agc caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc	848		
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Ala Pro Cys Gly			
215	220	225	
ctg gaa ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga aga agg	896		
Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg			
230	235	240	245
cca gtg cggtt aag aag gca aga gga gcc cca gtc cta gag	944		
Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu			
250	255	260	
aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac	992		
Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn			
265	270	275	
ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg	1040		
Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu			
280	285	290	
gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg	1088		
Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly			
295	300	305	
aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa	1133		
Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys			
310	315	320	
tagaaaacttt acagatgcta gtcccagaca taaaagaaaa taatgttctg gatgtgcacg	1193		
atggctcacg cctgtaatcc cagcactttg aggc当地agac gggtggatcg ctgagttcag	1253		
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Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr			
35	40	45	
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys			
50	55	60	
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser			
65	70	75	80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile			
85	90	95	

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr  
 100 105 110  
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe  
 115 120 125  
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp  
 130 135 140  
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu  
 145 150 155 160  
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala  
 165 170 175  
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln  
 180 185 190  
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser  
 195 200 205  
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu  
 210 215 220  
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu  
 225 230 235 240  
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly  
 245 250 255  
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro  
 260 265 270  
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln  
 275 280 285  
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser  
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 Ile Gln Glu Lys

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 <213> Artificial Sequence

<220>  
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<400> 19

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23

<210> 20  
 <211> 22  
 <212> DNA  
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<400> 20

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22

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aaaacattct ctctccccag cttcatgtg ttaacctggg g atg atg tgg acc tgg	Met Met Trp Thr Trp	176
	1 5	
gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg		224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu		
10 15 20		
cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat		272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Arg Lys Asn		
25 30 35		
tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac		320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr		
40 45 50		
aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca		368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr		
55 60 65		
acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt		416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu		
70 75 80 85		
cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa		464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu		
90 95 100		
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag		512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu		
105 110 115		
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt		560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val		
120 125 130		
ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg		608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu		
135 140 145		
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc		656
Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val		
150 155 160 165		
aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat		704
Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp		
170 175 180		
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat		752
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr		
185 190 195		
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac		800
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp		
200 205 210		
tgg agc caa gaa aaa atg gga atg act gag gaa gaa ggc aag cta ctc		848
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys Leu Leu		
215 220 225		

cct gcg att ccc gtc ctg tct gct ctg gtg tagggctgct ttgggctaga	898
Pro Ala Ile Pro Val Leu Ser Ala Leu Val	
230	235

cttgggtggg tttgtcacca cctgggtggg aatcatggaa tctcatgacc ccaggggccc	958
cctgtaccat cgagagttag cctgcacaac ttgtgcccc aaaggcaag gatcacattt	1018
taataactcat gaggttctta tactatacat gaaagggtat catabcattt gttttgtttt	1078
gttttgttt tgagatggag tcttactctg tcacccagga tggagtgcag ttagtgcac	1138
tcggctact gccaccacca cctcccgagt tcaagcaatt cttgtgcctc agcctccaa	1198
gtagctggga ttacaggggc ccacgaccat gcccgttga ttttgtatt ttttagtagag	1258
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accttgact cccaaagtgt tgggattaca ggcgtgagcc actgtgcccc gccagtgatca	1378
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 <212> PRT  
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Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr	
35 40 45	
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys	
50 55 60	
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser	
65 70 75 80	
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile	
85 90 95	
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr	
100 105 110	
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe	
115 120 125	
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp	
130 135 140	
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu	
145 150 155 160	
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala	
165 170 175	
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln	
180 185 190	
Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser	
195 200 205	
Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu	
210 215 220	
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225 230 235	

<210> 23  
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<220>  
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<210> 24		
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<223> Oligonucleotide primer ZC14063		
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<210> 26		
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<213> Artificial Sequence		
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<223> Oligonucleotide primer ZC17574		
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<211> 24		
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<210> 33	
<211> 30	
<212> DNA	
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Glu Tyr Met Pro Met Glu	
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<211> 8  
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 Asp Tyr Lys Asp Asp Asp Asp Lys  
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<210> 36  
 <211> 699  
 <212> DNA  
 <213> Homo sapiens

<400> 36

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acccctgagg	tcacatgcgt	gttggtgac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggta	tgacggcgt	ggaggtgc	aatgccaaga	caaagcccg	ggaggagcag	240
tacaacagca	cgtaccgtgt	gttcagcg	ctcaccgtcc	tgcaccagga	ctggctgaat	300
gcgcaaggagt	acaagtgc	gttctccaac	aaagccctcc	catcctccat	cgagaaaaacc	360
atctccaa	ccaaaggggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccg	420
gatgagctg	ccaagaacca	ggtcagcctg	acctgcctg	tcaaaggctt	ctatcccagc	480
gacatcgcc	tggagtggg	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccggtctgg	actccgacgg	ctccttctc	ctctacagca	agtcaccgt	ggacaagagc	600
aggtgtgc	aggggacgt	cttctcatgc	tccgtatgc	atgaggctct	gcacaaccac	660
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 <212> DNA  
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<220>  
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<400> 37

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1					5				10				15			

agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac  
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc  
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45

ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60

ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80

tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 288

85	90	95	
aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys 100 105 110			336
cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro 115 120 125			384
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 130 135 140			432
gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp 145 150 155 160			480
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 165 170 175			528
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu 180 185 190			576
cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 195 200 205			624
aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly 210 215 220			672
cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu 225 230 235 240			720
ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 245 250 255			768
ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 260 265 270			816
aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc Asn Tyr Lys Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe 275 280 285			864
ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 290 295 300			912
gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 305 310 315 320			960
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<210> 38  
 <211> 330  
 <212> PRT  
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 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45  
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60  
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80  
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95  
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110  
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 115 120 125  
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
 130 135 140  
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
 145 150 155 160  
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
 165 170 175  
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
 180 185 190  
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
 195 200 205  
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
 210 215 220  
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
 225 230 235 240  
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
 245 250 255  
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
 260 265 270  
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
 275 280 285  
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
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 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
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 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 325 330

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ttg aaa tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat	96
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr	
20 25 30	
ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg	144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser	
35 40 45	
ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc	192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	
50 55 60	
tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa	240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	
65 70 75 80	
cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc	288
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	
85 90 95	
gtc aca aag agc ttc aac agg gga gag tgt tag	321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *	
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Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser	
35 40 45	
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr	
50 55 60	
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys	
65 70 75 80	
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro	
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Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
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 aactgttagat ttcttaggaat tcaatccttg gccacgcgtc 100

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 <212> DNA  
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 aaaacattct ctctccccag cttcatgtg ttaacctggg g atg atg tgg acc tgg 176  
 Met Met Trp Thr Trp  
 1 5

gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224  
 Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu  
 10 15 20

cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272  
 Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Arg Lys Asn  
 25 30 35

tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320  
 Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr  
 40 45 50

aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368  
 Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr  
 55 60 65

acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt	416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu	
70 75 80 85	
cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa	464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu	
90 95 100	
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag	512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu	
105 110 115	
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt	560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val	
120 125 130	
ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg	608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu	
135 140 145	
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc	656
Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val	
150 155 160 165	
aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat	704
Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp	
170 175 180	
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat	752
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr	
185 190 195	
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac	800
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp	
200 205 210	
tgg agc caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc	848
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Ala Pro Cys Gly	
215 220 225	
ctg gaa ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga aga agg	896
Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg	
230 235 240 245	
cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc cta gag	944
Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu	
250 255 260	
aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac	992
Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn	
265 270 275	
ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg	1040
Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu	
280 285 290	
gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg	1088
Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly	
295 300 305	

aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa tca Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys Ser 310 315 320 325	1136
ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac cag cta Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu 330 335 340	1184
gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg atg att Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile 345 350 355	1232
gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu 360 365 370	1280
tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys 375 380 385	1328
cct ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys 390 395 400 405	1376
gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro 410 415 420	1424
tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val 425 430 435	1472
acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile 440 445 450	1520
tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser 455 460 465	1568
aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys 470 475 480 485	1616
cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt gct ggg Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser Ala Gly 490 495 500	1664
gga acc aac ggg acc agc ata aat ttc aag aca ttg tca ttc agt gtc Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe Ser Val 505 510 515	1712
ttt gag att atc ctc ata act tct ctg att ggt gga ggc ctt ctt att Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Leu Leu Ile 520 525 530	1760
ctc att atc ctg aca gtg gca tat ggt ctc aaa aaa ccc aac aaa ttg Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn Lys Leu 535 540 545	1808
act cat ctg tgt tgg ccc acc gtt ccc aac cct gct gaa agt agt ata Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser Ser Ile	1856

550	555	560	565	
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tct gat gac tct gtg aac aca gaa gac agg atc tta aaa cca tgt tcc Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser 585		590		1952
acc ccc agt gac aag ttg gtg att gac aag ttg gtg gtg aac ttt ggg Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly 600		605		2000
aat gtt ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu 615		620		2048
aac aat tta gga ggg gaa aag aat ggg act aga att ctg tct tcc tgc Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser Ser Cys 630		635		2096
cca act tca ata taagtgtgga ctaaaatgcg agaaaagggtgt cctgtggct Pro Thr Ser Ile				2148

atgcaaatta gaaaggacat gcagagttt ccaacttagga agactgaatc tggggccca agagaaccat ctctgaagac tgggtatgtg gtctttcca cacatggacc acctacggat gcaatctgtatgcatgcatgtgc atgagaagtc ttttattaaag tagatgtga aaacatggtt atggtaataag gaacagctt taaaatgtct ttgtatttgg gcctttcata caaaaaagcc ataataccat ttcatgttaa tgctatactt ctatactattt ttcatgttaat actataactt tatactattt tcatgttaata ctatacttct atactatttt catgttaatac tatacttcta tattaaagggtt ttacccactc a	2208
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	2388
	2448
	2508
	2529

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 <211> 649  
 <212> PRT  
 <213> Homo sapiens

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Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr 35		40	45	
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys 50		55	60	
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser 65		70	75	80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile 85		90	95	
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr 100		105	110	
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe 115		120	125	
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp 130		135	140	
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu 145		150	155	160
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala 165		170		175

Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln  
 180 185 190  
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser  
 195 200 205  
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu  
 210 215 220  
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu  
 225 230 235 240  
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly  
 245 250 255  
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro  
 260 265 270  
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln  
 275 280 285  
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser  
 290 295 300  
 Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala  
 305 310 315 320  
 Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val  
 325 330 335  
 Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val  
 340 345 350  
 Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr  
 355 360 365  
 Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln  
 370 375 380  
 Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro  
 385 390 395 400  
 Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala  
 405 410 415  
 Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile  
 420 425 430  
 Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu  
 435 440 445  
 Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly  
 450 455 460  
 Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly  
 465 470 475 480  
 Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala  
 485 490 495  
 Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr  
 500 505 510  
 Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly  
 515 520 525  
 Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys  
 530 535 540  
 Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro  
 545 550 555 560  
 Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys  
 565 570 575  
 Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile  
 580 585 590  
 Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu  
 595 600 605  
 Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala  
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<211> 1947
<212> DNA
<213> Artificial Sequence

<220>
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<221> misc_feature
<222> (1)...(1947)
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acntggwsnc cnggnaarga racnwsntay acncartaya cngtnaarmg nacntaygcn 180
tgyggngara arcaygayaa ytgyacnacn aaywsnwsna cnwsngaraa ymgngcnwsn 240
tgywsnttyt tyytnccnmg nathacnath ccngayaayt ayacnathga rgtngargcn 300
garaayggng ayggngtnat haarwsncay atgacntayt ggmgnytnga raayathgcn 360
aaracngarc cnccnaarat htymngntn aarccngtny tnngnathaa rmgnatgath 420
carathgart ggathaarcncc ngarytngcn ccngtnwsnw sngaytnaa rtayacnytn 480
mgnntymgna cngtnaayws nacnwsntgg atggargtna ayttycnnaa raaymgnaar 540
gayaaraayc aracntayaa yytnacnggn ytnccnccnt tyacngarta ygttnathgcn 600
ytnmgntgyg cngtnaarga rwsnaartty tggwsngayt ggwsncarga raaratgggn 660
atgacngarg argargcncc ntgyggnytn garytnntggm gngtnytnaa rccngcngar 720
gcngayggnm gnmgnccngt nmgnytntn tggaraaarg cnmgngngc nccngtnytn 780
garaaracny tnngntayaa yathgttay tayccngarw snaayacnaa ytnacngar 840
acnatgaaya cnacnaayca rcarytngar ytnccnccnt gngngarws nttytggtn 900
wsnatgathw sntayaayws nytnngnaar wsncnctng cnacnytnmg nathccngcn 960
athcargara arwsnttyca rtgyathgar gtnatgcarg cntgygtngc ngargaycar 1020
ytngtngtna artggcarws nwsngcnytng gaygttnaaya cntggatgt hgartggty 1080
ccngaygtng aywsngarcc nacnacnytn wsntgggarw sngtnwsnca rgcnacnaay 1140
tggacnathc arcargayaa rytnaarccn ttytggtyt ayaayathws ngtntayccn 1200
atgytncayg ayaargtngg ngarcntay wsnathcarg cntaygcnaa rgarggngtn 1260
ccnwsngarg gncngarac naargtngar aayathggng tnaaracngt nacnathacn 1320
tggaaargara thccnaarws ngarmgnaar ggnathath gyaaytayac nathttypay 1380
cargcngarg gngnaargg nttywsnaar acngtnaayw snwsnathyt ncrtaygg 1440
ytngarwsny tnaarmgnaa racnwsntay athgtncarg tnatggcnws nacnwsngcn 1500
gnggnacna ayggnacnws nathaaytta aaracnytnw snttywsngt nttygarath 1560
athytnatha cnwsnytnat hggngnggn ytnytnathy tnathathyt nacngtngcn 1620
tayggnytna araarcnnaa yaarytnacn caytntgtyt ggcncnacngt nccnaayccn 1680
gcngarwsnw snathgcna ntggcayggm gaygaytta argayaaryt naayttna 1740
garwsngayg aywsngtnaa yacngargay mgnathyttna arccntgyws nacnccnwsn 1800
gayaarytng tnathgayaa rytngtngtn aayttyggna aygtntnca rgaratht 1860
acngaygarg cnmgnacnng ncargaraay aaytngngn gngaraaraa yggnacnmgn 1920
athytnwsnw sntgyccnac nwsnath 1947

<210> 48
<211> 32
<212> PRT
<213> Homo sapiens

<400> 48
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Cys Pro Gln Asn Ile Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly
20 25 30

<210> 49
<211> 23
<212> DNA
<213> Artificial Sequence

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<210> 50  
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 <212> DNA  
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<220>  
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 <400> 50  
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<210> 51  
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<210> 52  
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 <212> PRT  
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<400> 52  
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<210> 53  
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 <212> DNA  
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 ttggctcaact gcaaccccttg cctcccccgtt tcaagcgatt ctcctgcctc agcctcccgaa 240  
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 cactttgact tgggctgggc ttaaaagcac aagaaaagct cgcagacaat cagagtggaa 360  
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 gttgctgtggg aggtggagtt gcctttgtatg caaatcctt gagccagcag aacatctgtg 480  
 gaacatcccc tgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg 532  
 Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu  
 1 5 10

ggg atg atg tgg acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa 580  
 Gly Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys  
 15 20 25

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tac tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa Tyr Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu 45 50 55 60	676
acc agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa Thr Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu 65 70 75	724
aaa cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct Lys His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala 80 85 90	772
tcg tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc Ser Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr 95 100 105	820
att gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg Ile Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met 110 115 120	868
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ttc cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa Phe Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu 145 150 155	964
tgg ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca Trp Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr 160 165 170	1012
ctt cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc Leu Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe 175 180 185	1060
gct aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg Ala Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu 190 195 200	1108
cag cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag Gln Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu 205 210 215 220	1156
tca aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag Ser Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu 225 230 235	1204
gaa gaa gct cca tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct Glu Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala 240 245 250	1252
gag gcg gat gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga Glu Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg 255 260 265	1300
gga gcc cca gtc cta gag aaa aca ctt ggc tac aac ata tgg tac tat	1348

Gly Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr				
270	275	280		
cca gaa agc aac act aac ctc aca gaa aca atg aac act act aac cag				1396
Pro Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln				
285	290	295	300	
cag ctt gaa ctg cat ctg gga ggc gag agc ttt tgg gtg tct atg att				1444
Gln Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile				
305	310	315		
tct tat aat tct ctt ggg aag tct cca gtg gcc acc ctg agg att cca				1492
Ser Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro				
320	325	330		
gct att caa gaa aaa tca ttt cag tgc att gag gtc atg cag gcc tgc				1540
Ala Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys				
335	340	345		
gtt gct gag gac cag cta gtg gtg aag tgg caa agc tct gct cta gac				1588
Val Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp				
350	355	360		
gtg aac act tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc				1636
Val Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro				
365	370	375	380	
acc acc ctt tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc				1684
Thr Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile				
385	390	395		
cag caa gat aaa tta aaa cct ttc tgg tgc tat aac atc tct gtg tat				1732
Gln Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr				
400	405	410		
cca atg ttg cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat				1780
Pro Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr				
415	420	425		
gcc aaa gaa ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac				1828
Ala Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn				
430	435	440		
att ggc gtg aag acg gtc acg atc aca tgg aaa gag att ccc aag agt				1876
Ile Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser				
445	450	455	460	
gag aga aag ggt atc atc tgc aac tac acc atc ttt tac caa gct gaa				1924
Glu Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu				
465	470	475		
ggt gga aaa gga ttc tcc aag aca gtc aat tcc agc atc ttg cag tac				1972
Gly Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr				
480	485	490		
ggc ctg gag tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg				2020
Gly Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met				
495	500	505		
gcc agc acc agt gct ggg gga acc aac ggg acc agc ata aat ttc aag				2068
Ala Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys				
510	515	520		

aca ttg tca ttc agt gtc ttt gag att atc ctc ata act tct ctg att	2116
Thr Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile	
525 530 535 540	
ggt gga ggc ctt ctt att ctc att atc ctg aca gtg gca tat ggt ctc	2164
Gly Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu	
545 550 555	
aaa aaa ccc aac aaa ttg act cat ctg tgt tgg ccc acc gtt ccc aac	2212
Lys Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn	
560 565 570	
cct gct gaa agt agt ata gcc aca tgg cat gga gat gat ttc aag gat	2260
Pro Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp	
575 580 585	
aag cta aac ctg aag gag tct gat gac tct gtg aac aca gaa gac agg	2308
Lys Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg	
590 595 600	
atc tta aaa cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag	2356
Ile Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys	
605 610 615 620	
ttg gtg gtg aac ttt ggg aat gtt ctg caa gaa att ttc aca gat gaa	2404
Leu Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu	
625 630 635	
gcc aga acg ggt cag gaa aac aat tta gga ggg gaa aag aat ggg act	2452
Ala Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr	
640 645 650	
aga att ctg tct tcc tgc cca act tca ata taagtgtgga ctaaaatgcg	2502
Arg Ile Leu Ser Ser Cys Pro Thr Ser Ile	
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Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg	
35 40 45	
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr	
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Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn	
65 70 75 80	
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe	

85	90	95														
Phe	Leu	Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	
100							105						110			
Ala	Glu	Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	
115							120					125				
Leu	Glu	Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	
130							135				140					
Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	
145							150				155			160		
Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	
165									170				175			
Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	
180								185				190				
Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	
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Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	
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Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Ala	Pro		
225					230					235			240			
Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	
245									250			255				
Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	
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Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn	
275							280				285					
Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu	
290						295					300					
His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser	
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325							330				335					
Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val	Ala	Glu	Asp	
340							345				350					
Gln	Leu	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	Asn	Thr	Trp
355							360				365					
Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	Thr	Leu	Ser	
370							375				380					
Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	Lys	
385					390					395			400			
Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro	Met	Leu	His	
405									410			415				
Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	Gly	
420							425				430					
Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile	Gly	Val	Lys	
435							440				445					
Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu	Arg	Lys	Gly	
450							455				460					
Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	Gly	
465							470				475			480		
Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly	Leu	Glu	Ser	
485										490			495			
Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	Ser	
500									505			510				
Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr	Leu	Ser	Phe	
515									520			525				
Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly	Gly	Leu		
530							535				540					
Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys	Lys	Pro	Asn	
545									550			555			560	
Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro	Ala	Glu	Ser	
565									570			575				
Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys	Leu	Asn	Leu	

580	585	590	
Lys Glu Ser Asp Asp Ser Val Asn Thr	Glu Asp Arg Ile Leu Lys Pro		
595	600	605	
Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp	Lys Leu Val Val Asn		
610	615	620	
Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp	Glu Ala Arg Thr Gly		
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Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly	Thr Arg Ile Leu Ser		
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athwsntgyg tntaytayta ymgnaraay ytnacn	cntggwsncc ngnnaargar	180
acnwsntaya cncartayac ngtnaarmgn acntaygc	tyggngaraa rcaygayaay	240
tgyacnacna aywsnwsnac nwsngaraay mngcnwsn	gywsn	300
athacnathc cngayaayta yacnathgar gtn	tyt ytnccnmgn	360
aarwsncaya tgacntaytg gmgnytngar aayathgcna	araayggnga yggngtnath	420
ttymgn	aracn	480
tnca	arathgartg gathaarcn	540
g	gnttymgnac ngt	600
acnwsntg	tnaaywsn	660
ga	ayaaraayca racntayaay	720
tggargt	tnmgn	780
tnca	ngt	840
wsnaarttyt ggw	tgacngarga rgargcnccn	900
tgyggnytng arytntggmg	ngt	960
mgnyt	ccngcngarg cngaygg	1020
ntnt	ngmncn	1080
ggaaraargc	ccngt	1140
athtgg	ntng	1200
tayt	g	1260
ayccngarws	tn	1320
carytngary tncayytn	gnacn	1380
ng	thc	1440
ytnggnaarw snccngt	arg	1500
tgyathgarg tnatgc	g	1560
wsngcnytng aygt	g	1620
acnacn	g	1680
sntgggarws ntgnws	g	1740
ytnaarc	g	1800
nt	g	1860
garc	g	1920
nt	g	1980
aargtngara	g	1986
garmgnaarg gnathat	g	
ttywsnaara cngt	g	
acnwsntaya thgtnc	g	
athaaytta aracn	g	
gngngny tnytn	g	
aarytnacnc ayytnt	g	
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ctctcagaga aggcagtgtt	ggaggcggtt ctggcccccggg	tctccctccta ctgttcctgg	180
tagcccgcc ttctcggggt	ggaaggagaa gctggccagg	tgagctctga ggaagc atg	239
		Met	
		1	
ctg agc agc cag aag gga tcc tgc agc cag gaa cca ggg gca gcc cac			287
Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala His			
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gtc cag cct ctg ggt gtg aac gct gga ata atg tgg acc ttg gca ctg			335
Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu			
20	25	30	
tgg gca ttc tct ttc ctc tgc aaa ttc agc ctg gca gtc ctg ccg act			383
Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro Thr			
35	40	45	
aag cca gag aac att tcc tgc ttt tac ttc gac aga aat ctg act			431
Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu Thr			
50	55	60	65
tgc act tgg aga cca gag aag gaa acc aat gat acc agc tac att gtg			479
Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile Val			
70	75	80	
act ttg act tac tcc tat gga aaa agc aat tat agt gac aat gct aca			527
Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala Thr			
85	90	95	
gag gct tca tat tct ttt ccc cgt tcc tgt gca atg ccc cca gac atc			575
Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp Ile			
100	105	110	
tgc agt gtt gaa gta caa gct caa aat gga gat ggt aaa gtt aaa tct			623
Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys Ser			
115	120	125	
gac atc aca tat tgg cat tta atc tcc ata gca aaa acc gaa cca cct			671
Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro Pro			
130	135	140	145
ata att tta agt gtg aat cca att tgt aat aga atg ttc cag ata caa			719
Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile Gln			
150	155	160	
tgg aaa ccg cgt gaa aag act cgt ggg ttt cct tta gta tgc atg ctt			767
Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met Leu			
165	170	175	
cggttc aga act gtc aac agt agc cgc tgg acg gaa gtc aat ttt gaa			815
Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe Glu			
180	185	190	

aac tgt aaa cag gtc tgc aac ctc aca gga ctt cag gct ttc aca gaa	863
Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr Glu	
195 200 205	
tat gtc ctg gct cta cga ttc agg ttc aat gac tca aga tat tgg agc	911
Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp Ser	
210 215 220 225	
aag tgg agc aaa gaa gaa acc aga gtg act atg gag gaa gtt cca cat	959
Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro His	
230 235 240	
gtc ctg gac ctg tgg aga att ctg gaa cca gca gac atg aac gga gac	1007
Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly Asp	
245 250 255	
agg aag gtg cga ttg ctg tgg aag aag gca aga gga gcc ccc gtc ttg	1055
Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu	
260 265 270	
gag aaa aca ttt ggc tac cac ata cag tac ttt gca gag aac agc act	1103
Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser Thr	
275 280 285	
aac ctc aca gag ata aac aac atc acc acc cag cag tat gaa ctg ctt	1151
Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu Leu	
290 295 300 305	
ctg atg agc cag gca cac tct gtg tcc gtg act tct ttt aat tct ctt	1199
Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser Leu	
310 315 320	
ggc aag tcc caa gag acc atc ctg agg atc cca gat gtc cat gag aag	1247
Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu Lys	
325 330 335	
acc ttc cag tac att aag agc atg cag gcc tac ata gcc gag ccc ctg	1295
Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro Leu	
340 345 350	
ttg gtg gtg aac tgg caa agc tcc att cct gcg gtg gac act tgg ata	1343
Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp Ile	
355 360 365	
gtg gag tgg ctc cca gaa gct gcc atg tcg aag ttc cct gcc ctt tcc	1391
Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu Ser	
370 375 380 385	
tgg gaa tct gtg tct cag gtc acg aac tgg acc atc gag caa gat aaa	1439
Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp Lys	
390 395 400	
cta aaa cct ttc aca tgc tat aat ata tca gtg tat cca gtg ttg gga	1487
Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu Gly	
405 410 415	
cac cga gtt gga gag ccg tat tca atc caa gct tat gcc aaa gaa gga	1535
His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly	
420 425 430	
act cca tta aaa ggt cct gag acc agg gtg gag aac atc ggt ctg agg	1583

Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu Arg			
435	440	445	
aca gcc acg atc aca tgg aag gag att cct aag agt gct agg aat gga			1631
Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn Gly			
450	455	460	465
ttt atc aac aat tac act gta ttt tac caa gct gaa ggt gga aaa gaa			1679
Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys Glu			
470	475	480	
ctc tcc aag act gtt aac tct cat gcc ctg cag tgt gac ctg gag tct			1727
Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu Ser			
485	490	495	
ctg aca cga agg acc tct tat act gtt tgg gtc atg gcc agc acc aga			1775
Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr Arg			
500	505	510	
gct gga ggt acc aac ggg gtg aga ata aac ttc aag aca ttg tca atc			1823
Ala Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser Ile			
515	520	525	
agt gtg ttt gaa att gtc ctt cta aca tct cta gtt gga gga ggc ctt			1871
Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly Leu			
530	535	540	545
ctt cta ctt agc atc aaa aca gtg act ttt ggc ctc aga aag cca aac			1919
Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro Asn			
550	555	560	
cgg ttg act ccc ctg tgt tgt cct gat gtt ccc aac cct gct gaa agt			1967
Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu Ser			
565	570	575	
agt tta gcc aca tgg ctc gga gat ggt ttc aag aag tca aat atg aag			2015
Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met Lys			
580	585	590	
gag act gga aac tct ggg aac aca gaa gac gtg gtc cta aaa cca tgt			2063
Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro Cys			
595	600	605	
ccc gtc ccc gcg gat ctc att gac aag ctg gta gtg aac ttt gag aat			2111
Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu Asn			
610	615	620	625
ttt ctg gaa gta gtt ttg aca gag gaa gct gga aag ggt cag gcg agc			2159
Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala Ser			
630	635	640	
att ttg gga gga gaa gcg aat gag tat atc tta tcc cag gaa cca agc			2207
Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro Ser			
645	650	655	
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Cys Pro Gly His Cys			
660			
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cttccttcatg cagagaccag gactagagcg gattcctcat gtttgccag gtcctcagt			2382
ccttgctcgg gtcaggatc ttcaacaatg cccttctgg gacactccat catccactta			2442

tat	ttttttttt	ttgcaacatt	gtggattgaa	cccagggact	tgtttatgcg	cgcaacttca	2502
gt	taactgtgg	cagagactta	ggaatggaga	tctgaccctt	tgcaagaagg	ttctggacat	2562
cc	cgccctgt	gtgagcctca	gacagcattg	tctttacttt	gaatcagctt	ccaagttaat	2622
aa	aaagaaaaaa	cagagagggt	gcataaacagc	tcctgcttcc	tgacctgtt	gagttccagt	2682
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 Leu Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro  
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 Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu  
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 Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile  
 65 70 75 80  
 Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala  
 85 90 95  
 Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp  
 100 105 110  
 Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys  
 115 120 125  
 Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro  
 130 135 140  
 Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile  
 145 150 155 160  
 Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met  
 165 170 175  
 Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe  
 180 185 190  
 Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr  
 195 200 205  
 Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp  
 210 215 220  
 Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro  
 225 230 235 240  
 His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly  
 245 250 255  
 Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val  
 260 265 270  
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 275 280 285  
 Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu  
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 305 310 315 320  
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 325 330 335  
 Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro  
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 Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu  
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Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu			
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Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu			
420	425	430	
Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu			
435	440	445	
Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn			
450	455	460	
Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Lys			
465	470	475	480
Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu			
485	490	495	
Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr			
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Arg Ala Gly Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser			
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Ile Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly			
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Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro			
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Asn Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu			
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Ser Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Ser Asn Met			
580	585	590	
Lys Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro			
595	600	605	
Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu			
610	615	620	
Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala			
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Ser Ile Leu Gly Gly Glu Ala Asn Glu Tyr Ile Leu Ser Gln Glu Pro			
645	650	655	
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&lt;211&gt; 21

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21

&lt;210&gt; 59

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC29082

&lt;400&gt; 59

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36

&lt;210&gt; 60

&lt;211&gt; 36

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&lt;213&gt; Artificial Sequence

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acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa ttc agc ctg gca		96
Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala		
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gct ctg cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg		144
Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg		
35                   40                   45		
aaa aat tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc		192
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr		
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cag tac aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat		240
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn		
65                   70                   75                   80		
tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt		288
Cys Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe		
85                   90                   95		
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Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu		
100                   105                   110		

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Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg	
115 120 125	
tta gag aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa	432
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys	
130 135 140	
cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct	480
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro	
145 150 155 160	
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Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg	
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Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg	
180 185 190	
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Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr	
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Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp	
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Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro	
225 230 235 240	
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Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly	
245 250 255	
aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc	816
Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val	
260 265 270	
cta gag aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac	864
Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn	
275 280 285	
act aac ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg	912
Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu	
290 295 300	
cat ctg gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct	960
His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser	
305 310 315 320	
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Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu	
325 330 335	
aaa tca ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac	1056
Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp	
340 345 350	
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Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp	

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ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val 565 570 575			1728
aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 580 585 590			1776
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 595 600 605			1824

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Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	
610 615 620	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc	1920
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val	
625 630 635 640	
tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc	1968
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala	
645 650 655	
aaa ggg cag ccc cga gaa cca cag gt <del>g</del> tac acc ctg ccc cca tcc cg <del>g</del>	2016
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg	
660 665 670	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc	2064
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly	
675 680 685	
ttc tat ccc agc gac atc gcc gt <del>g</del> gag tgg gag agc aat ggg cag cc <del>g</del>	2112
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro	
690 695 700	
gag aac aac tac aag acc acg cct ccc gt <del>g</del> ctg gac tcc gac ggc tcc	2160
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser	
705 710 715 720	
ttc ttc ctc tac agc aag ctc acc gt <del>g</del> gac aag agc agg tgg cag cag	2208
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln	
725 730 735	
ggg aac gtc ttc tca tgc tcc gt <del>g</del> atg cat gag gct ctg cac aac cac	2256
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His	
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tac acg cag aag agc ctc tcc ctg tct cc <del>g</del> ggt aaa taa	2295
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Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg	
35 40 45	
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr	
50 55 60	
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn	
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Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe	
85 90 95	
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu	

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130							135					140			
Pro	Val	Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro
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Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg
							165					170			175
Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg
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Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr
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Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp
							210					215			220
Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro
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Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly
							245					250			255
Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val
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Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn
							275					280			285
Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu
							290					295			300
His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser
							305					310			320
Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	Ile	Gln	Glu
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Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val	Ala	Glu	Asp
							340					345			350
Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	Asn	Thr	Trp
							355					360			365
Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	Thr	Leu	Ser
							370					375			380
Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	Lys
							385					390			400
Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro	Met	Leu	His
							405					410			415
Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	Gly
							420					425			430
Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile	Gly	Val	Lys
							435					440			445
Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu	Arg	Lys	Gly
							450					455			460
Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	Gly
							465					470			480
Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly	Leu	Glu	Ser
							485					490			495
Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala	Ser	Thr	Ser
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Ser	Val	Phe	Glu	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro
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Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe
							545					550			560
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
							565					570			575
Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe
							580					585			590
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro

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Val Leu His Gln Asp Trp	Leu Asn Gly Lys	Glu Tyr Lys Cys Lys Val	
625	630	635	640
Ser Asn Lys Ala Leu Pro Ser Ser	Ile Glu Lys Thr Ile Ser Lys Ala		
645	650	655	
Lys Gly Gln Pro Arg Glu Pro Gln	Val Tyr Thr Leu Pro Pro Ser Arg		
660	665	670	
Asp Glu Leu Thr Lys Asn Gln	Val Ser Leu Thr Cys Leu Val Lys Gly		
675	680	685	
Phe Tyr Pro Ser Asp Ile Ala Val	Glu Trp Glu Ser Asn Gly Gln Pro		
690	695	700	
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	Leu Asp Ser Asp Gly Ser		
705	710	715	720
Phe Phe Leu Tyr Ser Lys Leu Thr Val	Asp Lys Ser Arg Trp Gln Gln		
725	730	735	
Gly Asn Val Phe Ser Cys Ser Val	Met His Glu Ala Leu His Asn His		
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Tyr Thr Gln Lys Ser Leu Ser	Leu Ser Pro Gly Lys		
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<223> Oligonucleotide primer ZC29180

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<210> 73

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 ctctcagaga aggcaatgtgtgg ggaggcggttc ctggcccggtt tctccctccta ctgttcctgg 180  
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 Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu  
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Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys Ser	
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Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro Leu	
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Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys Glu			
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Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu Ser			
485	490	495	
ctg aca cga agg acc tct tat act gtt tgg gtc atg gcc agc acc aga			1775
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